1/9 DD4b5.3 Coding Sequence

Length 2563 bp

r	GGC	GCG	GCZ	AGG	rcg	GAGO	CTC		GCT					CTC	CTT	STG	GCC/	ACC	GTC	GCI						
•	R	G	Q	V	G	A	R	S	С	Ċ	F	W	F	s	С	G	Н	R	R	+ C	60					
61	GTC	GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA																								
V 2	P	A	A	L	G	С	R	T	D	ĸ	A	W	A	T	A	P	Q	K	P	T	120					
121	CGC	AGCI	CGA	ACGO	CAGO	GGC								SCG1	GTC	GGA	AGGG	GCG	CCG	CGC						
161	Q	L	ם	A	G	A	G	R	R	V	G	D	R	V	s	E	G	A	A.	+ R	180					
181		GGGCAGGCGGGGGGCGCCAGAGGGGGGAAAGAGGCGGGGGG															245									
101	А	G	G	R	A	D,	Ε	G	Ε	R	G	G	G	G	G	S	A	A	G	R	240					
241	GGGC	CGG	CGG	GGG	AAI	GTC	GAT						GCI	GCC	:CGG	GGT	'CGG	GGA	AGG	AGC						
241	A	G	G	G	М	S	М	p	D	A	М	P	L	P	G	V	G	E	Ε	+ L	300					
301	TGAA	AGCA	GGC	CAA	AGGA	GAT	'CGA	GGA	CGC	CGA	GAA	GTA	CTC	CTT	CAT	GGC	CAC	:CGI	CAC	CA						
301	ĸ	Q	A	K	E	I	E	D	A	E	K	Y	s	F	М	A	T	v	T	K	360 -					
361	AGGC	GCC	CAA	GAA	.GCA	AAT	CCA	GTI	TGC	TGA	TGA	CAT	GCA	.GGA	GTT	CAC	CAA	ATI	ccc	CA						
201	A	P	K	К	Q	I	Q	F	Α	D	D	М	Q	Ε	F		K	F	P	+ T	420 -					
421	CCAA														CTC	CAC	TGA	CAG	CTA	CA						
441	K	T	+ G	R	R	s	+ L	s	R	-+- S	I	S	Q	s	s	 T	+ D	s	Y	-+ S	480 -					
481	GTTC	AGC	TGC	ATC	CTA	CAC	AGA	TAG	CTC	TGA	TGA	TGA	GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGAGTTTCTCCCCGAGAGAAGCAGC													
401							4			,											_					
	S	Α	A	s	Y	T	+ D	s	s	_+- D	D	 Е	+	 s	 P	 R	+ E	K	Q	-+ Q	540					
5 <i>h</i> 1	AAAC		CTC	CAA	.GGG		CAG	S CAA	s TTT	D CTG	D TGT	E GAA	v GAA	s	 P	R	+ E		Q	Q						
541			CTC	CAA	.GGG	T CAG S	CAG	S CAA	s TTT	D CTG	D TGT	E GAA	v GAA	s	 P	R	+ E		Q	Q	540 - 600					
	AAAC T GACG	CAA N	CTC + S GGA	CAA K	.GGG	 S	CAG + S	S CAA N N	S TTT F GCA	D CTG -+- C AGA	TGT V CAT	E GAA K GTC	V GAA + N TGC	S CAT	P CAA K	R GCA Q	+ E GGC + A	K AGA E	Q ATT	Q TG -+ G						
541	AAAC T GACG	CAA N	CTC + S GGA	CAA K	.GGG	 S	CAG + S	S CAA N N	S TTT F	D CTG -+- C AGA	TGT V CAT	E GAA K GTC	V GAA + N TGC	S CAT	P CAA K	R GCA Q	+ E GGC + A	K AGA E	Q ATT	Q TG -+ G						
601	AAAC T GACG	CCG R	CTC + S GGA + E	CAA K GAT	GGG G TGA	S GAT	CAG + S TGC + A	S CAA N AGA E GGC	S TTT F GCA Q TGG	CTG C C AGA TGC	TGT V CAT M	E GAA K GTC S	V GAA N TGC + A	CAT I TCT L	P CAA K GAT	R GCA Q TTC	GGC + A ACT + L	K AGA E CAG	Q ATT F GAA K	TG G AC R	600					
	AAAC T GACG	CCG R TCA	CTC + S GGA + E	CAA K GAT	GGG G TGA	S GAT	CAG + S TGC + A	S CAA N AGA E GGC	S TTT F GCA	CTG C C AGA TGC	TGT V CAT M	E GAA K GTC S	V GAA N TGC + A	CAT I TCT L	P CAA K GAT	R GCA Q TTC	GGC + A ACT + L	K AGA E CAG	Q ATT F GAA K	TG G AC R	600					
601	AAAC T GACG R GTGC	CAA N CCG R TCA	CTC + S GGA + G	CAA K GAT I GGA	GGG GTGA EGAA	GAT I GCC	CAG + S TGC + A CTT + L	S CAA N AGA E GGC A	S TTT F GCA TGG G	CTG AGA TGC A CTG	TGT V CAT M TAA K TGC	E GAA K GTC S AAT	GAA N TGC A AGT V GGG	S CAT I TCT L GGG	P CAA K GAT I CTG	R GCA Q TTC S TAC	GGC + ACT + L ACA + H	K AGA E CAG R	Q ATT F GAA K CAC	TG -+ G AC -+ R AG -+ A	600					
601	AAAC T GACG R GTGC	CAA N CCG R TCA	CTC + S GGA + G	CAA K GAT I GGA	GGG GTGA EGAA	GAT I GCC	CAG + S TGC + A CTT + L	S CAA N AGA E GGC A	S TTT F GCA TGG G	CTG AGA TGC A CTG	TGT V CAT M TAA K TGC	E GAA K GTC S AAT	GAA N TGC A AGT V GGG	S CAT I TCT L GGG	P CAA K GAT I CTG	R GCA Q TTC S TAC	GGC + ACT + L ACA + H	K AGA E CAG R	Q ATT F GAA K CAC	TG -+ G AC -+ R AG -+ A	600					
601 661 721	AAAC T GACG R GTGC A CCCA Q CTTG	CAA N CCG R TCA GAC	CTC+ S GGA+ GGGG+ A CAT	CAA K GAT I GGA E GGT V	GGGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	S GAT I GCC P GAT I	CAG + S TGC + A CTT + L TGA +	S CAA N AGA E GGC A GAC	S TTT F GCA TGG ACT L TGA	D CTG C AGA -+- D TGC -+- C AGT	TGT V CAT M TAA K TGC A	E GAA K GTC S AAT I CCT	GAA N TGC A AGT V GGG	S CAT I TCT L GGG	P CAA K GAT I CTG	R GCA Q TTC S TAC	GGC + ACT + ACA + H CCG	K AGA E CAG R CAT I	Q ATT F GAA K CAC T GTC	TG -+ G AC -+ A TG -+ A	600 - 660 - 720					
601	AAAC T GACG R GTGC A CCCA	CAA N CCG R TCA GAC	CTC+ S GGA+ GGGG+ A CAT	CAA K GAT I GGA E GGT V	GGGGT E GAA GTT L CTC	S GAT I GCC P GAT I	CAG + S TGC + A CTT + L TGA +	S CAA N AGA E GGC A GAC	S TTT F GCA TGG ACT L TGA	D CTG C AGA -+- D TGC -+- C AGT	TGT V CAT M TAA K TGC A	E GAA K GTC S AAT I CCT	GAA N TGC A AGT V GGG	S CAT I TCT L GGG GGC	P CAA K GAT I CTG	R GCA Q TTC S TAC	GGC ACA ACA ACA ACA ACA ACA ACA ACA ACA	K AGA E CAG R CAT I	Q ATT F GAA K CAC T GTC	TG -+ G AC -+ A TG -+ A	600 - 660 - 720					
601661721781	AAAC T GACG R GTGC A CCCA Q CTTG	CAA N CCG R TCA GAC T TAA	CTC+ S GGA+ GGG A CAT-	CAA K GAT I GGA E GGT V CTA	GGGGGTGAAGGAAGGGAAGGGGGGGGGGGGGGGGGGGG	GAT GCC P GAT I AAC T	CAG + S TGC + L TGA + E TCA + Q	S CAA N AGA E GGC A GAC T GAA N	S TTT F GCA Q TGG ACT L TGA	D CTG C AGA CTG C AGT.	TGT V CAT M TAA K TGC A AGC	E GAA K GTC S AAT I CCT L	V GAA N TGC A AGT V GGG AGC A A	S CAT I TCT L GGG G GC A ACT L	P CAA K GAT I CTG C TCAC	R GCA Q TTC T GTG C rGA	GGC+A ACT+L ACA+H CCG+R GGC+A	K AGA E CAG R CAT I CTG W TGG	Q ATT F GAA K CAC T GTC S AGT	TG+G AC+R AG+A TG+A	600 - 660 - 720 - 780					
601 661 721	AAAC T GACG R GTGC A CCCA Q CTTG C	CAA N CCG R TCA GAC T TAA	CTC+ S GGA+ GGG A CAT-	CAA K GAT I GGA E GGT V CTA	GGGGGTGAAGGAAGGGAAGGGGGGGGGGGGGGGGGGGG	S GAT I GCC P GAT I AAC	CAG + TGC + L TGA + TCA + Q	S CAA N AGA E GGC A GAC T GAA N	S TTT F GCA Q TGG ACT L	D CTG -+- AGA -+- CTG AGT V AGA	TGT V CAT M TAA K TGC A AGC	E GAA K GTC S AAT I CCT L TGC	GAA N TGC A AGT V GGG AGC A CTG	S CAT I TCT L GGG	P CAA K GAT I CTG C TCAC	R GCA Q TTC T GTG C rGA	GGC+A ACT+L ACA+H CCG+R GGC+A	K AGA E CAG R CAT I CTG W TGG	Q ATT F GAA K CAC T GTC S AGT	TG+G AC+R AG+A TG+A TG	600 - 660 - 720 - 780					
601661721781	AAAC T GACG R GTGC A CCCA Q CTTG C CAGT	CAA N CCG R TCA GAC T TAA	GGG GGA GGG AGC ACAT ACAT ACAT	CAA K GAT I GGA E GGT V CTA Y TTG	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAT GGGG	CAG + TGC + L TGA + CGAG +	S CAA N AGA E GGC A GAC T GAA N	S TTT F GCA Q TGG ACT L TGA E AGA	D CTG C AGA C AGT. AGA	TGT V CAT M TAA TGC A TGA TGA	E GAA K GTC S AAT I CCT L TGC. A CTT F	GAA N TGC A AGT V GGG AGC. A CTGG	S CAT I TCT L GGG A ACT U GTGG	P CAA K GAT I CTG C TCAC	R GCA Q TTC S TAC T GTG C TGA T T T	GGC+A ACT+L ACA+A CCG+A GGC+A	K AGA E CAG R TGG	Q ATT F GAA K CAC T GTC S AGT V CTG	TG+G AC+R AG+A TG+A TG+V	600 - 660 - 720 - 780 - 840					

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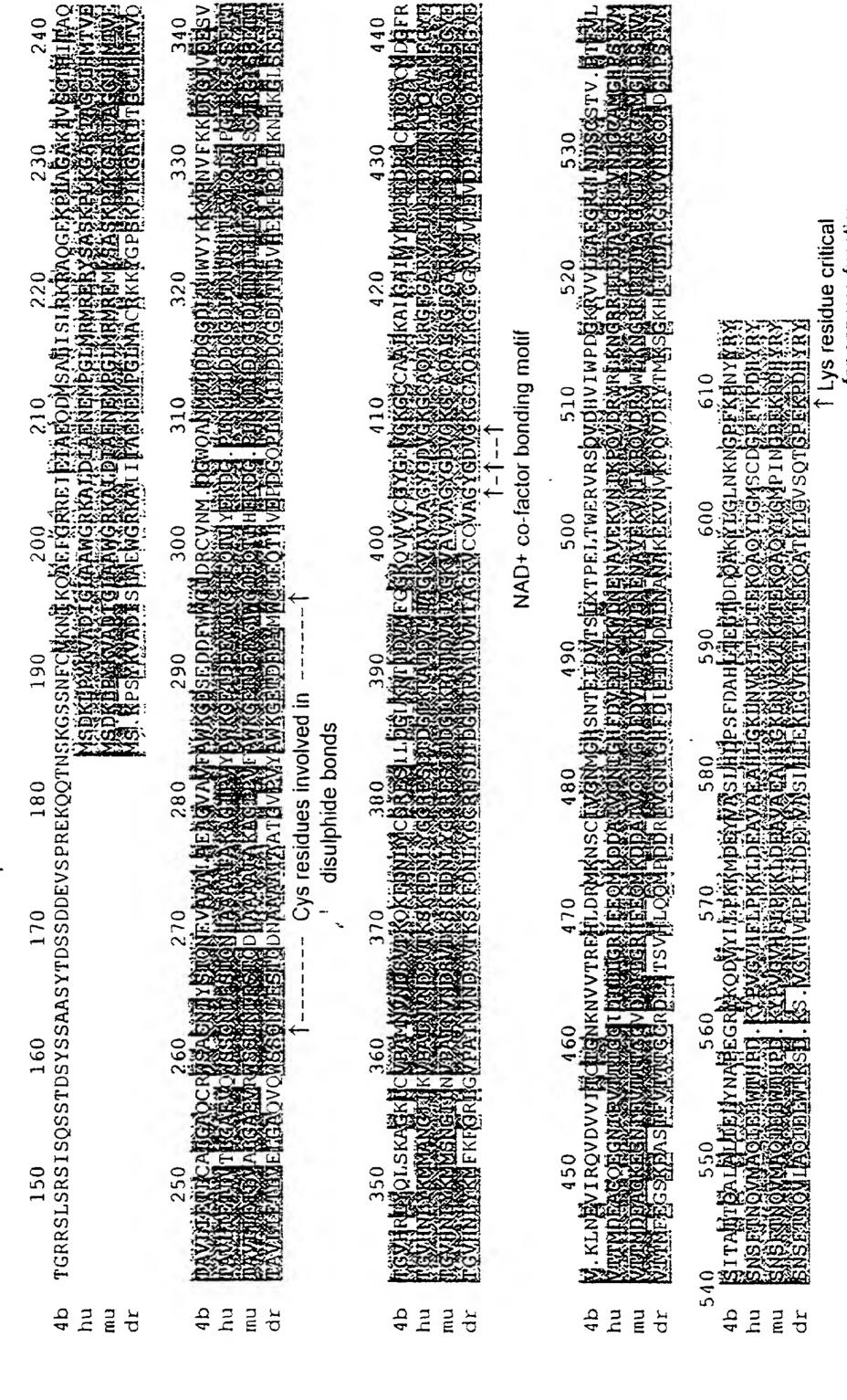
									<i>2</i> /:									C 3 C	· n .~ c										
961	GGGTT	CAT	CAAC	AA(STA?	rcc <i>i</i>								AGGC			SGA.P ⊦	GAC	AGC	.G	1020								
	V	Y	ĸ	K	Y	P	N	V	F	K	K	I	R	G	I	V	E	E	S	V	-								
1021	TGACT	rgg:	rgt:		CAG													CCC	GCC	CA -+	1080								
	T	G	V	Н	R	L	Y	Q	Ļ	S	K	A	G	K	L	С	V	P	A	M	-								
1081	TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAAT													1140															
	N	v	N	D	s	V	T	ĸ	Q	K	F	D	N	L	Y	С	С	R	E	S	-								
1141	CCAT		-														ACAZ			GG -+	1200								
	I	L	D	G	L	K	R	T	T	D		M	F	G	G	K	Q	V	V	V									
	TGTG'	rgg	CTA'	rgg'	TGA	GGT	AGG	CAA	GGG	CTG	CTG'	rgc:	rgc:	CT	CAA	AGC'	rct:	rgg/	AGC2		1260								
1201	С	G	Y	G	E	V		K	G	C	С	A	A	L	K	A	L	G	A	ĭ	-								
	TTGT																				1320								
1261	V	Y	I	 T	E			P	I	C	A	L	Q	A	С	M	D	G	F	R	-								
	GGGT	GGT	AAA	GCT	AAA	TGA	AGT																						
1321	v	 V	+ К	 L	 N	 E	+	 I	R	-+- Q	v	D	v	v	- 	 T	+	T	G	N	1380								
	ATAA	GAA	TGT	AGT	GAC	ACG	GGA	GCA	CTT	GGA	TCG	CAT	GAA	AAA	CAG	TTG	TAT	CGT	ATG	CA									
1381			+ V		T	 R	+ E	 Н	 L	-+- D	 R	 М	+ K	 N	 S		+	v	C	-+ N	1440								
	ATAT	GGG	CCA	.CTC	CAA	CAC	:AGA	AAT	CGA	TGT	GAC	CAG	CCT	CCG	CAC	TCC	GGA	GCT	GAC	GT									
1441		G	+ H	 s	. – – – N	 Т	+ E	 I		-+- V	 T	 S	+ L	 R	 T	 P	+ E	 L	 T	-+ W	1500								
	GGGA	-		_		· ጥ		CGA		тст	ירב מר		הככ	AGA	тсс	CAA	ACG	AGT	TGT	CC									
1501			+				· 			-+- V			+ P		 G		+ R			-+ T.	1560 -								
	E	R	٧	R	S	Q	V	D	H 	·	7		•	_	_		•		v 	~=									
1561	TCCT	'GGC	AGA	GGG	TCG	TCI		'CAA			CTG					CAC		TGT	TCT	GT -+	1620								
	L	A	E	G	R	L	L	N	L	\$	С	S	T	V	P	T	F	V	L	S									
1621	CCAT	CAC	AGC	CAC	CAAC	ACA	AGGC	TTT			'GAT				TAA	TGC	ACC	CGA	.GGG	GC -+	1680								
1621	I	T	A	T	T	Q	A	L	A	L	I	E	L	Y	N	A	P	E	G	R	_								
	GATA	CAP	AGCA	AGGI	ATGI	rgta	ACTI	GC1	TC	TA	AGAF	raa <i>i</i>	GGP	ATGA	ATA	CGI	TGC	CAG	CTT	GC	1740								
1681	Y	K	Q	D	٧	Y	-+ L	L	P	K	K	М	D	E	Y	V	A	s	L	H	1740								
	ATCI	rgcc	CATO	CAT	rtga	atg(CCCI	ACCI	TAC	CAG	AGCI	GAC	CAGA	ATGA	ACCA	AGC	CAAA				1800								
1741		P	s	F	D	A	-+ H	L	T	E	L	 T	Đ	D	Q	A	K												
	GACT	rca <i>i</i>	ACA/	LAA	ATG																								
1801	L	N															-+			+	1860								
10.31	CAAG	GGA(CCA	STC	CAC																1920								
1801				·																									
1921	TTT		CTT	ACT +	CCT'	TTC	-+-														1980								
1981	TCA'				-									CATO							2040								

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2041	GAAGIICAGGGICCCICACICIAGICACIAAAGAAGGAIIIIACICCCCCAGCCCAGAAA	2100
2101	GGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA	2160
2161	GGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGA	2220
2221	GCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGT	2280
2281	ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA	2340
2341	AGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGG	2400
2401	CTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCCACCA	2460
2461	GACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTAATTTTGTCC	2520
2521	TCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAA	

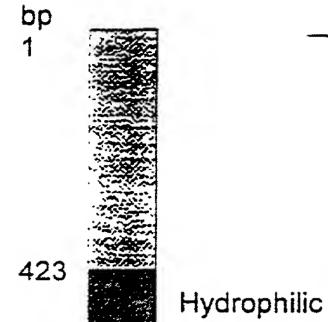
FIG 1 (Cont)

with full-length AHCY amino acid sequences of human (hu), mouse (mu) and drosophila (dr) in portant for AHCY function Noted are conserved features shown to b Alignment of DD4b5.3 AHCY-like domain



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DD4b5.3 sequence schematic



No significant similarity to database sequences.

Of the 50 amino acids in the hydrophillic domain, 38 residues are hydrophilic by the Kyle and Doolittle hydropathy index, including 16 serine residues.

Domain 573

Has 52% amino acid similarity to human AHCY sequences and shares many conserved features, including seven of eight cysteine residues, a co-factor binding motif and a lysine shown by in-vitro mutagenesis studies to be critical for AHCY function

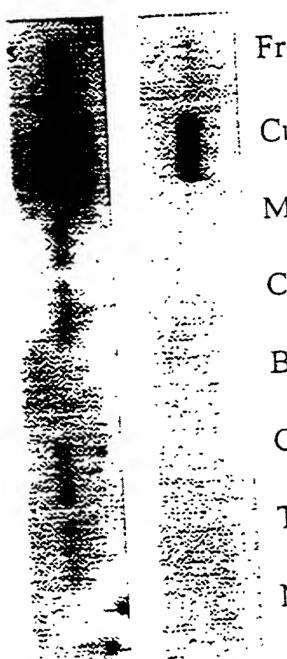
AHCY-like Domain

1845

3' Untranslated Region

2563

Southern blot analysis of DD4b5.3 RT-PCR results



Fresh DC (Mix⁻, DR⁺)

Cultured DC (CMRF44⁺)

Monocytes (CD14+)

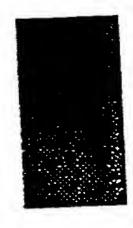
Cultured Monocytes (CD14+)

Blymphocytes (CD19⁺)

Cultured B Lymphocytes (CD19+)

T Lymphocytes (CD3⁺)

NK Cells (CD16+, CD57+)





L428

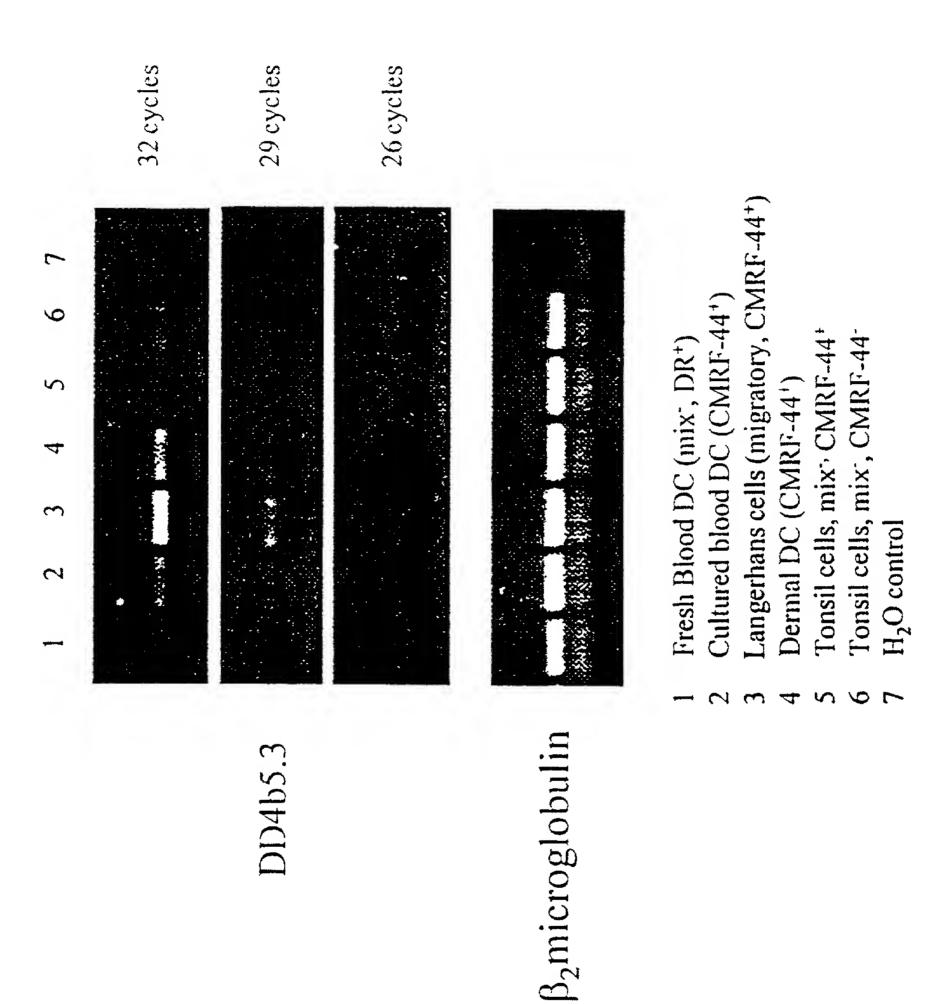
L428 RT-

60 minutes exposure

1 minute exposure

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Expression of DD4b5.3 in DC lineage panel, as assessed by RT-PCR



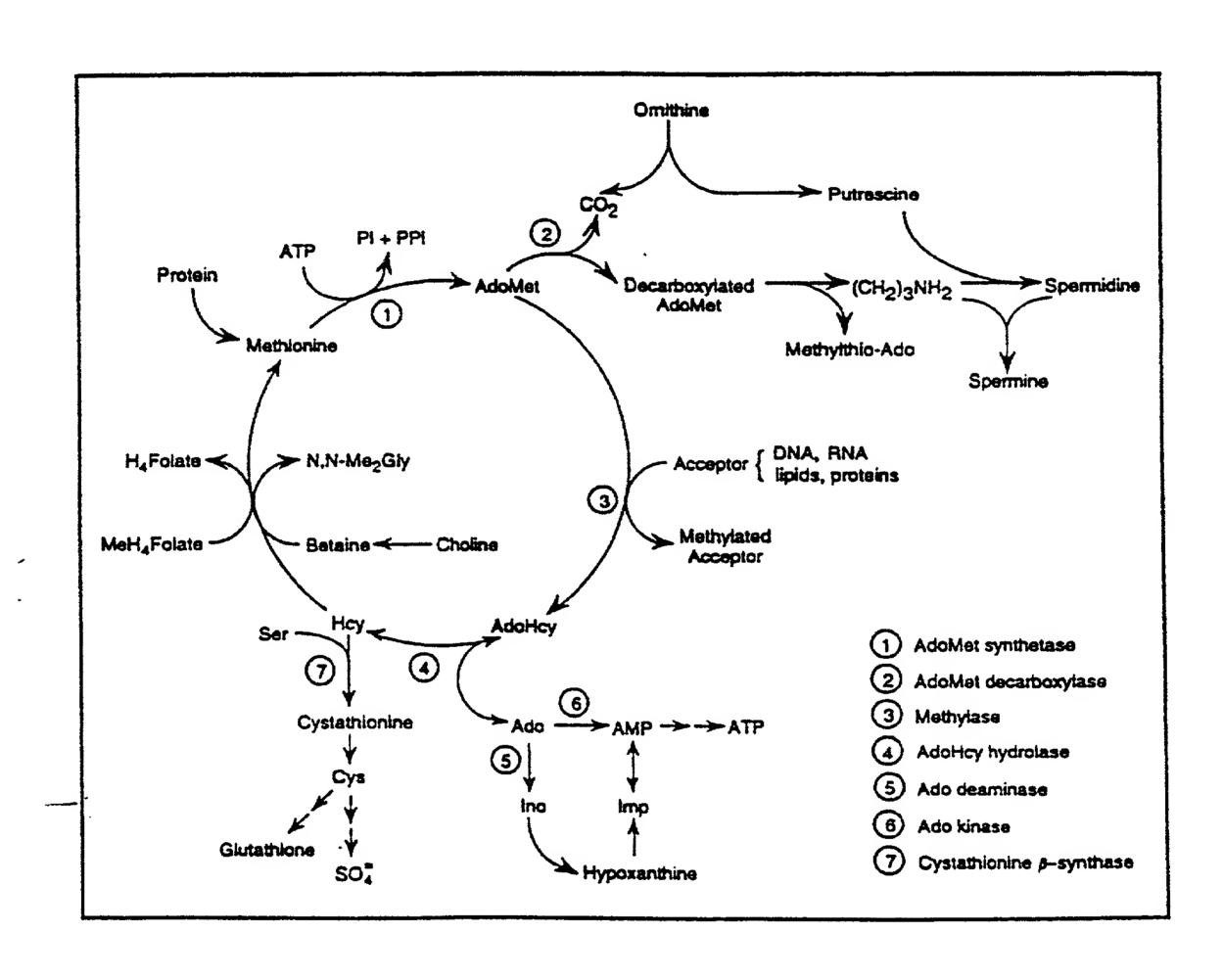


FIG 6

ilm b

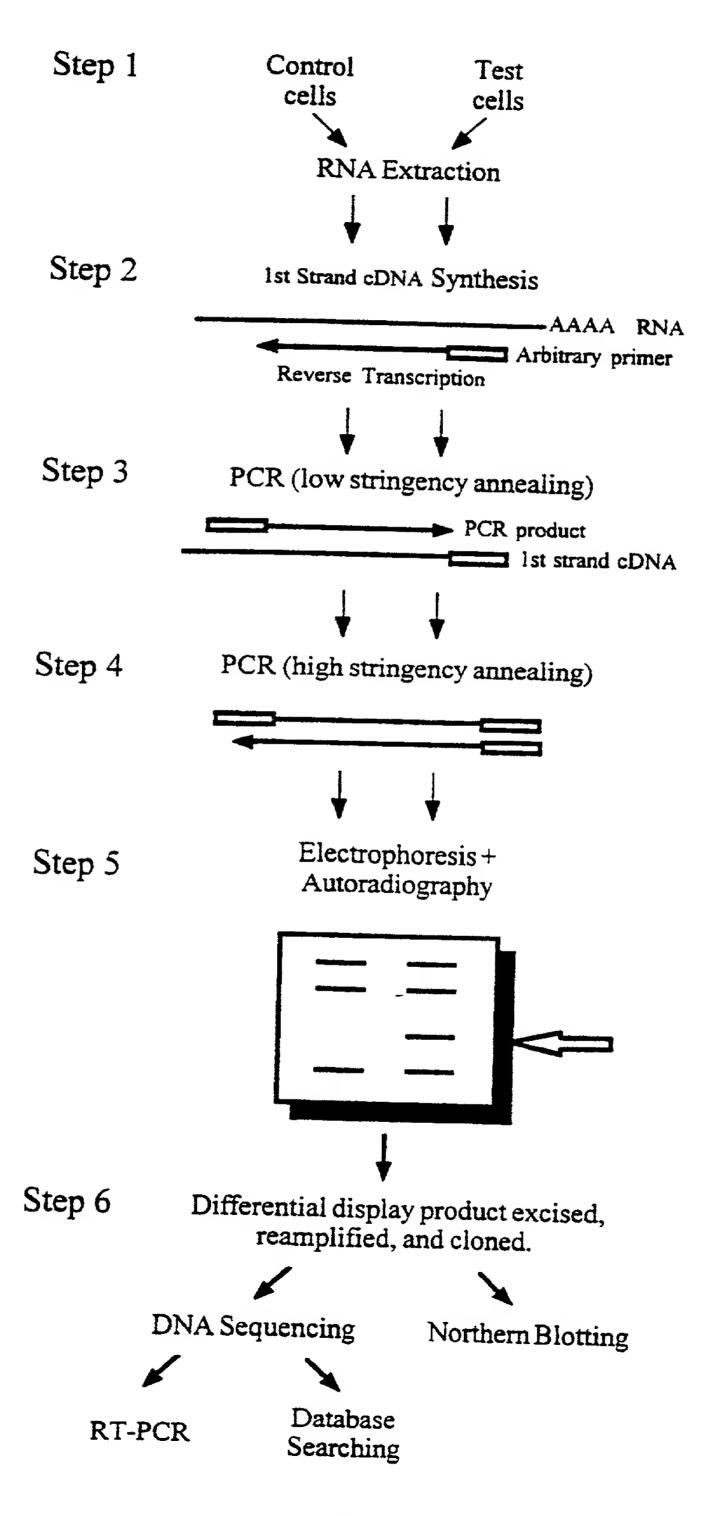


FIG 7